

Package: ofhsyn (via r-universe)

June 10, 2026

Type Package

Title Synthetic Our Future Health Data Generator

Version 0.1.1

Author Hannah Nicholls [aut, cre]

Maintainer Hannah Nicholls <h.l.nicholls@qmul.ac.uk>

Description Generates synthetic Our Future Health cohort datasets for method development, including participant, questionnaire, clinic measurements, outpatient, inpatient, emergency, mortality, primary care medication, and geography outputs. Supports reproducible generation with configurable cohort size and user-defined International Classification of Diseases, Tenth Revision (ICD-10), Office of Population Censuses and Surveys Classification of Interventions and Procedures, version 4 (OPCS-4), and British National Formulary (BNF) code pools.

License MIT + file LICENSE

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Depends R (>= 4.2.0)

Imports methods, utils, stats

Suggests testthat (>= 3.0.0), knitr, rmarkdown

VignetteBuilder knitr

Config/testthat/edition 3

Repository <https://hlnicholls.r-universe.dev>

Date/Publication 2026-06-04 15:43:03 UTC

RemoteUrl <https://github.com/hlnicholls/ofhsyn>

RemoteRef HEAD

RemoteSha 1a378db61f2815d818c2d9ffe98bc326bc9d328f

Contents

| | |
|---------------------------------|---|
| generate_ofh_cohort | 2 |
| generation_primitives | 3 |
| ofh_build_config | 4 |
| OFHCohortSynthesizer | 5 |

| | |
|--------------|----------|
| Index | 7 |
|--------------|----------|

| | |
|---------------------|---|
| generate_ofh_cohort | <i>Generate Synthetic OFH Cohort Datasets</i> |
|---------------------|---|

Description

Generate linked synthetic health datasets for a configurable cohort.

Usage

```
generate_ofh_cohort(
  n = 5000,
  seed = 42,
  icd10 = NULL,
  icd10_file = NULL,
  opcs4 = NULL,
  opcs4_file = NULL,
  bnf_codes = NULL,
  bnf_codes_file = NULL,
  proportions = NULL,
  record_multipliers = NULL,
  code_config = NULL,
  save_csv = TRUE,
  return_objects = TRUE,
  output_dir = NULL
)
```

Arguments

| | |
|------------|---|
| n | Total synthetic cohort size. |
| seed | Random seed. |
| icd10 | Optional named character vector of ICD-10 descriptions. |
| icd10_file | Optional path to a TXT/CSV file containing ICD-10 code and description pairs. TXT format should be tab-separated with code and description columns. CSV format should provide code and description columns. |
| opcs4 | Optional named character vector of OPCS-4 descriptions. |
| opcs4_file | Optional path to a TXT/CSV file containing OPCS-4 code and description pairs. TXT format should be tab-separated with code and description columns. CSV format should provide code and description columns. |

| | |
|---------------------------------|--|
| <code>bnf_codes</code> | Optional BNF input for primary care meds. Can be either a character vector of BNF codes or a data frame with columns for code, name, and formulation (optional strength). |
| <code>bnf_codes_file</code> | Optional path to a TXT/CSV file for BNF input. TXT supports one BNF code per line. CSV supports either code-only or structured medication rows containing code, name, and formulation (optional strength). |
| <code>proportions</code> | Optional named list of dataset-level coverage proportions. Names should match <code>names(ofh_default_proportions())</code> . |
| <code>record_multipliers</code> | Optional named list of multipliers for multi-record datasets. Names should match <code>names(ofh_default_record_multipliers())</code> . |
| <code>code_config</code> | Optional nested list overriding field-level code generation probabilities and pools. Structure should follow <code>ofh_default_code_config()</code> . |
| <code>save_csv</code> | Whether to write CSV outputs to disk. |
| <code>return_objects</code> | Whether to return generated data frames as an R object. |
| <code>output_dir</code> | Output directory when <code>save_csv = TRUE</code> . |

Value

Named list of generated data frames when `return_objects = TRUE`; otherwise invisible NULL.

Acknowledgement

We extend our thanks to GitHub user [@icallumwebb](#) for contributing a bug fix that improved custom code handling.

Examples

```
out <- generate_ofh_cohort(n = 200, seed = 123, save_csv = FALSE, return_objects = TRUE)
names(out)
```

`generation_primitives` *Standalone Synthetic Generation Primitives*

Description

Utility functions for generating participant populations and event-level synthetic records.

Usage

```
generate_ofh_population(n = 1000, seed = 123)

add_inpatient_events(
  data,
  events_per_person = 5,
  icd10_codes = c("I210", "I500", "I639", "E110", "J440"),
```

```

opcs4_codes = c("K401", "K451", "K561", "M011", "E033"),
seed = 123
)

synthesize_drug_exposure(
  data,
  drug_list = c("0212000B0", "0601023A0"),
  seed = 123,
  mean_items_per_person = 2
)

```

Arguments

| | |
|-----------------------|---|
| data | Input data frame containing a pid column. |
| n | Number of participants. |
| seed | Random seed. |
| events_per_person | Mean events per participant. |
| icd10_codes | ICD-10 code pool. |
| opcs4_codes | OPCS-4 code pool. |
| drug_list | Medication code pool. |
| mean_items_per_person | Mean prescription items per participant. |

Value

Return value depends on the function called:

`generate_ofh_population()` Data frame with one row per participant and columns including pid, sex, and birth_year.

`add_inpatient_events()` Data frame of synthetic inpatient events with columns pid, admidate, icd10, and opcs4.

`synthesize_drug_exposure()` Data frame of synthetic primary-care medication records with participant IDs and prescribing/dispensing fields (for example prescribedbnfcode, paidbnfcode).

ofh_build_config

Configuration Helpers for OFH Generation

Description

Helper functions that return default settings and compose full generation configuration lists.

Usage

```

ofh_default_proportions()
ofh_default_record_multipliers()
ofh_default_code_config()
ofh_build_config(
  n = 5000,
  proportions = ofh_default_proportions(),
  record_multipliers = ofh_default_record_multipliers(),
  code_config = list()
)

```

Arguments

| | |
|--------------------|--|
| n | Total cohort size. |
| proportions | Dataset proportions list. |
| record_multipliers | Record multiplier list for event datasets. |
| code_config | Optional code configuration overrides. |

Value

Return value depends on the function called:

ofh_default_proportions() Named numeric list of dataset proportions in [0, 1].

ofh_default_record_multipliers() Named numeric list of multipliers for multi-record datasets.

ofh_default_code_config() Nested named list containing default code pools, weights, and generation controls by dataset.

ofh_build_config() Named list with total_pid_count (integer), datasets (nested list of dataset sizing settings), and code_config (merged code configuration list).

OFHCohortSynthesizer *Reference Class for OFH Cohort Generation*

Description

Reference class API for configuring and running synthetic cohort generation.

Usage

```
OFHCohortSynthesizer
```

Details

Create an instance with `OFHCohortSynthesizer$new(...)` and run generation via `$run_all(n = ...)`.

Value

A ReferenceClass generator object. Use `OFHCohortSynthesizer$new(...)` to create an instance. Instance methods return the instance invisibly for chaining where applicable, and `$run_all()` returns a named list of data frames when `return_objects = TRUE` (otherwise invisible `NULL`).

Examples

```
syn <- OFHCohortSynthesizer$new(project_root = ".", seed = 123)
out <- syn$run_all(n = 100, save_csv = FALSE, return_objects = TRUE)
```

Index

add_inpatient_events
 (generation_primitives), 3

generate_ofh_cohort, 2

generate_ofh_population
 (generation_primitives), 3

generation_primitives, 3

ofh_build_config, 4

ofh_default_code_config
 (ofh_build_config), 4

ofh_default_proportions
 (ofh_build_config), 4

ofh_default_record_multipliers
 (ofh_build_config), 4

OFHCohortSynthesizer, 5

synthesize_drug_exposure
 (generation_primitives), 3